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ILLINOIS INSTITUTE OF TECHNOLOGY

SIXTY-NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS

<130> 1310-1279

<140> 19-490,361

<141> 1310-01-07

0160-41

<170> PatentIn Ver. 2.1

0010-1

0011-1335

0012-DNA

0013-Homo sapiens

0020-

0021-gene

0022-(1)..(2335)

0020-

0021-CDS

0022-(183)..(2170)

0030-1

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cgcccccggc ccggccggcc cc atg gac gag acc ccc ccg cgc cgc ctc ggc 112
Met Ala Glu Ala Pro Pro Arg Arg Leu Gly
1 5 10

ctt ttt ccc ccg acc ggg gac gac acc ccg ccg gag ctg gtg ggc ctc 160
Leu Gly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu
15 20 25

acc gcc gtg ttt agc gaa cag ggc gag ccg ccg ggg ggc ggc tcc ccg 208
Thr Ala Val Glu Ser Gln Gly Glu Ala Gly Gly Gly Ser Pro
30 35 40

ccg ccg ctc ggc ctc ctg ggc acc ccc ctg ccg ccg ggc ggg ccc ctc 256
Arg Arg Leu Gly Leu Leu Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu
45 50 55

cct ggg ccg ggc tcc ggc tcg ggc tcc gcc tgc ggc cag ccg tcc tcc 304
Pro Gly Pro Gly Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser
60 65 70

gcc ccg ccc aac ccg tac ccg ccg ctg cag aac tgg gtc tac aac gtg 352
Ala Ala His Lys Arg Tyr Arg Arg Leu Gln Asn Trp Val Tyr Asn Val
75 80 85 90

ctt gag ccg ccc ccg ggc tgg gcc ttc gtc tac ccc gtc ttc ata ttt 400



... Ile Arg Pro Asn Ile Asp Ile Val Tyr His Val Ile Ile Pro				
atg ttt atc ttg aat tgg gtc ttg aat ttt atc ttt atc ttt Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Leu Ser Thr Ile Ile	111	115	121	445
cag lac cag gaa att gcc aac gag ttt atc atc ttt gaa ttt wrg Glu His Glu Leu Ala Asn Glu Cys Leu Leu Ile Leu Glu Phe Val	125	131	135	490
atg att gtg att ttt ggc ttg gag tac att gtc cgg gtc tgg tcc ucc Met Ile Val Val Phe Gly Leu Glu Tyr Ile Val Arg Val Trp Ser Ala	145	148	157	544
ggc tgc tgc tgc cgc tac cya gga tgg cag ggt cgc ttc cgc ttt gcc Gly Cys Cys Cys Arg Tyr Arg Gly Trp Glu Gly Arg Phe Arg Phe Ala	155	160	165	592
aga aag ccc ttc tgt gtc atc gag ttc att gtc ttc gtg gcc tcc gtg Arg Lys Pro Phe Cys Val Ile Asp Phe Ile Val Phe Val Ala Ser Val	175	180	185	640
gcc gtc atc gcc ggc ggt acc cag ggc aac atc ttc gcc acg tcc gcg Ala Val Ile Ala Ala Gly Thr Glu Gly Asn Ile Phe Ala Thr Ser Ala	190	195	200	688
ctg cgc agc atg cgc ttc ctg cag atc ctg cgc atg gtg cgc atg gac Leu Arg Ser Met Arg Phe Leu Glu Ile Leu Arg Met Val Arg Met Asp	205	210	215	736
cgc cgc ggc acc tgg aag ctg ctg ggc tca gtg gtc tac gcg cat Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val Val Tyr Ala His	220	225	230	784
acc aag gag ctg atc acc gcc tgg tac atc ggg ttc ctg gtg ctc atc Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile	235	240	245	832
ctc gcc tcc ttc ctg gtc tac ctg gcc gag aag gac gcc aac tcc gac Phe Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp	255	260	265	880
tcc tcc tcc tac gcc gag tgg tcc tgg ggg acg att aca ttg aca Phe Ser Ser Tyr Ala Asp Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr	270	275	280	924
acc att ggc tat ggt gag aag aca ccc gag aca tgg ctg ggc agg gtc Thr Ile Gly Tyr Gly Asp Lys Thr Pro His Thr Trp Leu Gly Arg Val	285	290	295	976
ctg gct gct ggc ttc gcc tta ctg ggc atc ttt ttc ttt gcc ctg cct Leu Ala Ala Gly Phe Ala Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro	300	305	310	1024
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 1 5 10 15
 Asp Ala Pro Arg Ala Glu Leu Val Ala Leu Thr Ala Val Gln Ser Glu
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 Gln Gly Glu Ala Gly Gly Ser Pro Arg Arg Leu Gly Leu Leu
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 Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu Pro Gly Pro Gly Ser Gly

Met Ala Glu Asp Val Ile Ala Ser Tyr Ser Ala Gly His Leu
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 Asp Asp Lys Lys Asp Val Ile Ser Leu Gln Thr Arg Val Asp Gln Ile
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 Val Gly Arg Gly Pro Gly Asp Arg Lys Ala Arg Gln Lys Gly Asp Lys
 140 145 150
 Val Ser Asp Ala Glu Val Val Asp Glu Ile Ser Met Met Gly Arg
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 Val Val Lys Val Glu Lys Gln Val Gln Ser Ile Glu His Lys Leu Asp
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Ser Gly Ala Tyr Gly Glu Asn Thr Ser Ala Ala His Lys Arg Tyr
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 Arg Arg Leu Glu Asn Trp Val Tyr Asn Val Leu Glu Arg Ile Arg Lys
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 Trp Ala Phe Val Tyr His Val Phe Ile Phe Leu Leu Val Phe Ser Phe
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 Leu Val Leu Ser Val Leu Ser Thr Ile Glu Glu His Glu Glu Leu Ala
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 Asn Glu Cys Leu Leu Ile Leu Glu Phe Val Met Ile Val Val Phe Gly
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 130 135 140
 Leu Glu Tyr Ile Val Arg Val Trp Ser Ala Gly Cys Cys Cys Arg Tyr
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 135 140 145
 Arg Gly Trp Glu Gly Arg Phe Arg; Ile Ala Arg Lys Pro Phe Cys Val
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 145 150 155
 Ile Asp Phe Ile Val Phe Val Ala Ser Val Ala Val Ile Ala Ala Gly
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 150 155 160
 Thr Glu Gly Asn Ile Phe Ala Thr Ser Ala Leu Arg Ser Met Arg Phe
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 165 170 175
 Leu Glu Ile Leu Arg Met Val Arg Met Asp Arg Arg Gly Gly Thr Trp
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 180 185 190
 Lys Leu Leu Gly Ser Val Val Tyr Ala His Ser Lys Glu Leu Ile Thr
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 195 200 205
 Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile Phe Ala Ser Phe Leu Val
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 210 215 220
 Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp Phe Ser Ser Tyr Ala Asp
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 Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp
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 Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser
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 270 275 280
 Gly Phe Ala Leu Lys Val Glu Glu Gln His Arg Gln Lys His Phe Glu
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 Lys Arg Arg Met Pro Ala Ala Asn Leu Ile Glu Ala Ala Trp Arg Leu
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 295 300 305
 Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu Thr Ala Thr Trp Tyr Tyr
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 310 315 320
 Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu Leu Ala Leu Leu Phe Glu
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 His Val Glu Arg Ala Arg Asn Gly Leu Arg Pro Leu Glu Val Arg
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 395 400 405
 Pro Ser Ser Glu Glu Val Gly Glu Ala Thr Ser Pro Thr Lys Val Glu
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 410 415 420
 Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg Phe Arg Ala Ser Leu Arg
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 425 430 435
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 440 445 450
 500 505 510

Ala Lys Ser Tyr Ala Lys Glu Leu Ile Val Asp Asp Ile Met Ile
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Ala Val Lys Thr Val Ile Arg Ser Ile Arg Ile Leu Lys Pro Ile Val
626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641
Ala Lys Arg Lys Ile Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys Asp
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Val Ile Glu Glu Tyr Ser Ala Gly His Leu Asp Met Leu Gly Arg Ile
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Lys Ser Leu Glu Thr Arg Val Asp Glu Ile Val Gly Arg Gly Pro Gly
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Asp Arg Lys Ala Arg Glu Lys Gly Asp Gly Pro Ser Asp Ala Glu
690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705
Val Val Asp Glu Ile Ser Met Met Gly Arg Val Val Lys Val Glu Lys
706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721
Gln Val Gln Ser Ile Glu His Lys Leu Asp Leu Leu Leu Gly Phe Tyr
722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737
Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala Ser Leu Gly Ala Val Gln
738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753
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<223> Description of Artificial Sequence: PCR Primer

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

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<213> Artificial Sequence

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<210> 6
Capillary Primer 1

<211> 6
Capillary Primer 1

<211> 6
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<214>
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<213> Artificial Sequence

<214>
<220> Description of Artificial Sequence: PCR Primer

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<422> 12

<423> 21

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<425> Artificial Sequence

<426>

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<429> tgcacatgtatg ggcagacctc c

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<430> 13

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<438> 14

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<412> Description of Artificial Sequence: PCR Primer

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<417> Artificial Sequence

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<423> Description of Artificial Sequence: PCR Primer

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<413> Artificial Sequence

<421>

<423> Description of Artificial Sequence: PCR Primer

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<412> PRT

<413> Homo sapiens

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Tyr Tyr Ile Val Ser Leu Glu Ile Ala Arg Gly Asp Ala Asp Gly
 4 4

Ala Ile Tyr Ala Pro Ile Ala Pro Gly Ala Pro Gly Ile Ala Pro Pro
 5 5 5

Ala Ser Pro Ala Ala Pro Ala Ala Pro Pro Val Ala Ser Asp Leu Gly
 60 70 75 80 85 90

Pro Arg Pro Pro Val Ser Leu Asp Pro Arg Val Ser Ile Tyr Ser Thr
 95 105 115 125

Arg Arg Pro Val Leu Ala Arg Thr His Val Gln Gly Arg Val Tyr Asn
 130 135 140

Phe Ile Glu Arg Pro Thr Gly Trp Lys Cys Phe Val Tyr His Phe Ala
 115 120 125

Val Phe Leu Ile Val Leu Val Cys Leu Ile Phe Ser Val Leu Ser Thr
 130 135 140

Ile Glu Gin Tyr Ala Ala Leu Ala Thr Gly Thr Leu Phe Trp Met Glu
 145 150 155 160

Ile Val Leu Val Val Phe Phe Gly Thr Glu Tyr Val Val Arg Leu Trp
 165 170 175

Ser Ala Gly Cys Arg Ser Lys Tyr Val Gly Leu Trp Gly Arg Leu Arg
 180 185 190

Phe Ala Arg Lys Pro Ile Ser Ile Ile Asp Leu Ile Val Val Val Ala
 195 200 205

Ser Met Val Val Leu Cys Val Gly Ser Lys Gly Gln Val Phe Ala Thr
 210 215 220

Ser Ala Ile Arg Gly Ile Arg Phe Leu Gln Ile Leu Arg Met Leu His
 225 230 235 240

Val Asp Arg Gln Gly Gly Thr Trp Arg Leu Leu Gly Ser Val Val Phe
 245 250 255

Ile His Arg Gln Glu Leu Ile Thr Thr Leu Tyr Ile Gly Phe Leu Gly
 260 265 270

Leu Ile Phe Ser Ser Tyr Phe Val Tyr Leu Ala Glu Lys Asp Ala Val
 275 280 285

Asn Glu Ser Gly Arg Val Glu Phe Gly Ser Tyr Ala Asp Ala Leu Trp
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Trp Gly Val Val Thr Val Thr Ile Gly Tyr Gly Asp Lys Val Pro
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Gln Thr Trp Val Gly Lys Thr Ile Ala Ser Cys Phe Ser Val Phe Ala
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Pro Ser Gln Ala Arg Lys Val Asn Thr Gln Leu Asp Gln Arg Leu Ala
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 Gln Asn Pro Asp Ser Ser Thr Trp Lys Ile Tyr Ile Arg Lys Ala Pro
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 Arg Arg Leu Asp Gln Ser Ile Gly Lys Pro Ser Leu Phe Ile Ser Val
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 Ser Glu Lys Ser Lys Asp Arg Gly Ser Asn Thr Ile Gly Ala Arg Leu
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 Asn Arg Val Glu Asp Lys Val Thr Gln Leu Asp Gln Arg Leu Ala Leu
 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985
 Ile Thr Asp Met Leu His Gln Leu Leu Ser Leu His Gly Gly Ser Thr
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Asn Thr Ile Pro Thr Tyr Ser Asn Leu Thr Val Pro Asn Asn Gly Pro
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Asp His Gly Ser
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<211> PRT

<213> Homo sapiens

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Asp Ser Thr Arg Asp Gly Ala Leu Ile Ala Gly Ser Glu Ala Pro
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
210 215 220

Val Ile Asn His Ser Ile Val Leu Val Thr Ala Trp Ile Ile Val Pro
 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400
 Leu Lys Leu Ile Ile Ala Ser Phe Ile Val Tyr Leu Ala Glu Lys Gly
 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480
 Ala Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540
 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355
 Asn Ile Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320
 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385
 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400
 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415
 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430
 Val Pro Met Tyr Arg Leu Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu
 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445
 Arg Asn Leu Lys Ser Lys Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro
 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460
 Pro Glu Pro Ser Pro Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe
 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480
 Ser Ser Pro Arg Gly Val Ala Ala Lys Gly Lys Ser Pro Gln Ala
 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495
 Gln Thr Val Arg Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser
 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510
 Pro Ser Lys Val Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala
 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
 Arg Gln Ala Phe Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu
 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540
 Glu Ala Ser Leu Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro
 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560
 Cys Glu Phe Val Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile
 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575
 Arg Ala Val Cys Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys
 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590

Val Asp Leu Arg Phe Tyr Asp Val Met Asp Val Ile Glu Val Pro Ser
 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Ala Gly His Leu Asp Met Ile Ser Arg Ile Lys Ser Leu Glu Ser Arg
 145 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Val Asp Gln Ile Val Gly Arg Phe Pro Ala Ile Thr Asp Lys Asp Arg
 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Thr Lys Gly Pro Ala Glu Ala Glu Leu Pro Glu Asp Pro Ser Met Met
 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Gly Arg Leu Gly Lys Val Glu Lys Gln Val Leu Ser Met Glu Lys Lys
 545 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Leu Asp Phe Leu Val Asn Ile Tyr Met Gln Arg Met Gly Ile Pro Pro
 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Thr Glu Thr Glu Ala Tyr Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro
 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Pro Tyr His Ser Pro Glu Asp Ser Arg Glu His Val Asp Arg His Gly
 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Cys Ile Val Lys Ile Val Arg Ser Ser Ser Ser Thr Gly Gln Lys Asn
 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Phe Ser Ala Pro Pro Ala Ala Pro Pro Val Gln Cys Pro Pro Ser Thr
 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Ser Trp Gln Pro Gln Ser His Pro Arg Gln Gly His Gly Thr Ser Pro
 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Val Gly Asp His Gly Ser Leu Val Arg Ile Pro Pro Pro Pro Ala His
 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Glu Arg Ser Leu Ser Ala Tyr Gly Gly Asn Arg Ala Ser Met Gln
 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Phe Leu Arg Gln Glu Asp Thr Pro Gly Cys Arg Pro Pro Glu Gly Thr
 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Leu Arg Asp Ser Asp Thr Ser Ile Ser Ile Pro Ser Val Asp His Gln
 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830

Glu Leu Glu Arg Ser Phe Ser Gly Phe Ser Ile Ser Gln Ser Lys Gln
 770 775 780 785 790 795 800 805 810 815 820 825 830

Asn Leu Asp Ala Leu Asn Ser Cys Tyr Ala Ala Val Ala Pro Cys Ala
 785 790 795 800 805 810 815 820 825 830

Lys Val Arg Pro Tyr Ile Ala Gln Gly Glu Ser Asp Thr Asp Ser Asp
 805 810 815 820 825 830

Leu Cys Thr Pro Cys Gly Pro Pro Arg Ser Ala Thr Gly Glu Gly
 820 825 830

Ile Pro Gly Asp Val Gly Thr Ala Gly Pro Asp Lys

111 112

113 114

115 116 PBT

117 118 HMM. suslets

119 120 121

Met Gly Leu Lys Ala Arg Arg Ala Ala Gly Ala Ala Gly Gly Gly
1 5 10 15

Asp Gly Gly Gly Gly Gly Ala Ala Asn Pro Ala Gly Gly Asp
20 25 30

Ala Ala Ala Ala Gly Asp Glu Glu Arg Lys Val Gly Leu Ala Pro Gly
35 40 45

Asp Val Glu Gln Val Thr Leu Ala Leu Gly Ala Gly Ala Asp Lys Asp
50 55 60

Gly Thr Leu Leu Leu Glu Gly Gly Arg Asp Glu Gly Gln Arg Arg
65 70 75 80

Thr Pro Gln Gly Ile Gly Leu Leu Ala Lys Thr Pro Leu Ser Arg Pro
85 90 95

Val Lys Arg Asn Asn Ala Lys Tyr Arg Arg Ile Gln Thr Leu Ile Tyr
100 105 110

Asp Ala Leu Glu Arg Pro Arg Gly Trp Ala Leu Leu Tyr His Ala Leu
115 120 125

Val Phe Leu Ile Val Leu Gly Cys Leu Ile Leu Ala Val Leu Thr Thr
130 135 140

Phe Lys Glu Tyr Glu Thr Val Ser Gly Asp Trp Leu Leu Leu Glu
145 150 155 160

Thr Phe Ala Ile Phe Ile Phe Gly Ala Glu Phe Ala Leu Arg Ile Trp
165 170 175

Ala Ala Gly Cys Cys Cys Arg Tyr Lys Gly Trp Arg Gly Arg Leu Lys
180 185 190

Phe Ala Arg Lys Pro Leu Cys Met Leu Asp Ile Phe Val Leu Ile Ala
195 200 205

Ser Val Pro Val Val Ala Val Gly Asn Gln Gly Asn Val Leu Ala Thr
210 215 220

Ser Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met Leu Arg Met
225 230 235 240

Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Ala Ile Cys Ala

His Ile Lys Ser Leu Ile Val Ala Trp Tyr Ile Glu, the last two lines
are

Ile Leu Ser Ser Ile Leu Val Tyr Ile Val Glu Lys Asp Val Pro Phe
375 376 377 378 379 380

Val Asp Ala Asn Gly Asn Glu Met Lys Glu Glu Phe Glu Thr Tyr Ala
381 382 383 384 385 386 387 388

Asp Ala Ile Trp Trp Gly Leu Ile Thr Leu Ala Thr Ile Gly Tyr Gly
389 390 391 392 393 394 395 396

Asp Lys Thr Pro Lys Thr Trp Glu Gly Arg Leu Ile Ala Ala Thr Phe
397 398 399 400 401 402 403 404

Ser Leu Ile Gly Val Ser Phe Ala Leu Pro Ala Gly Ile Leu Gly
405 406 407 408 409 410 411 412

Ser Gly Leu Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe
413 414 415 416 417 418 419 420

Glu Lys Arg Arg Lys Pro Ala Ala Glu Leu Ile Gln Ala Ala Trp Arg
421 422 423 424 425 426 427 428

Tyr Tyr Ala Thr Asn Pro Asn Arg Ile Asp Leu Val Ala Thr Trp Arg
429 430 431 432 433 434 435 436

Phe Tyr Glu Ser Val Val Ser Phe Pro Phe Phe Arg Lys Glu Gln Leu
437 438 439 440 441 442 443 444

Glu Ala Ala Ser Ser Gln Lys Leu Gly Leu Leu Asp Arg Val Arg Leu
445 446 447 448 449 450 451 452

Ser Asn Pro Arg Gly Ser Asn Thr Lys Gly Lys Leu Phe Thr Pro Leu
453 454 455 456 457 458 459 460

Asn Val Asp Ala Ile Glu Glu Ser Pro Ser Lys Glu Pro Lys Pro Val
461 462 463 464 465 466 467 468

Gly Leu Asn Asn Lys Glu Arg Phe Arg Thr Ala Phe Arg Met Lys Ala
469 470 471 472 473 474 475 476

Tyr Ala Phe Trp Gln Ser Ser Glu Asp Ala Gly Thr Gly Asp Pro Met
477 478 479 480 481 482 483 484

Ala Glu Asp Arg Gly Tyr Gly Asn Asp Phe Pro Ile Glu Asp Met Ile
485 486 487 488 489 490 491 492

Pro Thr Leu Lys Ala Ala Ile Arg Ala Val Arg Ile Leu Gln Phe Arg
495 496 497 498 499 500 501 502

Leu Tyr Lys Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys
503 504 505 506 507 508 509 510

Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Ser Arg

Ile Lys Tyr Asn Val Ile Asp Met Ile Phe Thr Ile Gly Ile
 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Pro Ser Thr Pro Lys His Lys Lys Ser Gln Lys Gly Ser Ala Ala Thr
 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Phe Pro Ser Gln Gln Ser Pro Arg Asp Asn Ala Pro Lys Val Ala Arg Pro
 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Ser Thr Ser Gln Ile Glu Asp Gln Ser Met Met Gly Lys Phe Val Lys
 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Val Glu Arg Gln Val Gln Asp Met Gly Lys Lys Leu Asp Phe Leu Val
 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Asp Met His Met Gln His Met Glu Arg Leu Gln Val Gln Val Thr Glu
 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Tyr Tyr Pro Thr Lys Gly Thr Ser Ser Pro Ala Glu Ala Glu Lys Lys
 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Glu Asp Asn Arg Tyr Ser Asp Leu Lys Thr Ile Ile Cys Asn Tyr Ser
 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Glu Thr Gly Pro Pro Glu Pro Pro Tyr Ser Phe His Gln Val Thr Ile
 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Asp Lys Val Ser Pro Tyr Gly Phe Phe Ala His Asp Pro Val Asn Leu
 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Pro Arg Gly Gly Pro Ser Ser Gly Lys Val Gln Ala Thr Pro Pro Ser
 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Ser Ala Thr Thr Tyr Val Glu Arg Pro Thr Val Leu Pro Ile Leu Thr
 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Leu Leu Asp Ser Arg Val Ser Cys His Ser Gln Ala Asp Leu Gln Gly
 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Pro Tyr Ser Asp Arg Ile Ser Pro Arg Gln Arg Arg Ser Ile Thr Arg
 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Asp Ser Asp Thr Pro Leu Ser Leu Met Ser Val Asn His Glu Glu Leu
 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Glu Arg Ser Pro Ser Gly Phe Ser Ile Ser Gln Asp Arg Asp Asp Tyr
 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880

Val Phe Gly Pro Asn Gly Gly Ser Ser Trp Met Arg Glu Lys Arg Tyr
 820 825 830 835 840 845 850 855 860 865 870 875 880

Leu Ala Glu Gly Glu Thr Asp Thr Asp Thr Asp Pro Phe Thr Pro Ser
 835 840 845 850 855 860 865 870 875 880

Gly Ser Met Pro Leu Ser Ser Thr Gly Asp Gly Ile Ser Asp Ser Val

Primer File Set Artificial:

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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21

<210> 37
<211> 21
<212> DNA
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<223> Description of Artificial Sequence: PCR Primer

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21

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21

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23

<210> 40
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<41> Artificial Sequence

<42> Description of Artificial Sequence: PCR Primer

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<44> Description of Artificial Sequence

<45> 41

<46> 24

<47> DNA

<48> Artificial Sequence

<49>

<50> Description of Artificial Sequence: PCR Primer

<51> 41

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24

25